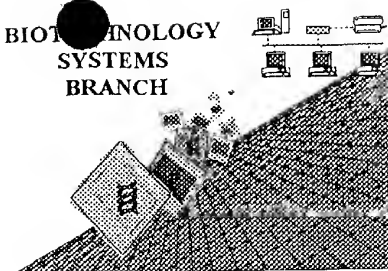


J. Souma

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/724,678

Source: 1655

Date Processed by STIC: 5-3-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/724,678

DATE: 05/03/2001
TIME: 21:17:44

INPUT SET: S36627.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

SEQUENCE LISTING

Does Not Comply
Corrected Diskette Needed

pp. 1, 2, 3

(1) General Information

(i) APPLICANTS: Kang-Hung Lee
Chi-Horng Bair
Yang-Yuan Tseng
Yih-Weng Wang
Shing-Hwan Wang

(ii) TITLE OF THE INVENTION: METHODS FOR DETECTING AND DIFFERENTIATING
ENTEROVIRUSES AND THE PRIMERS AND PROBES THEREFOR

(iii) NUMBER OF SEQUENCES: 11

Number of sequences differ:

- 11 listed

- 16 shown → see bottom of

page 3.

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Kolisch, Hartwell, Dickinson, McCormack & Heuser
(B) STREET: 520 SW Yahmill, Suite 200
(C) CITY: Portland
(D) STATE: Oregon
(E) COUNTRY: USA
(F) ZIP: 97204

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE:

Software type mandatory

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 28-Nov-2000

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Charles H. DeVoe
(B) REGISTRATION NUMBER: 37,305
(C) REFERENCE/DOCKET NUMBER: TAI 3L6

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (503) 224-6655
(B) TELEFAX: (503) 295-6679

RAW SEQUENCE LISTING PATENT APPLICATION US/09/724,678

DATE: 05/03/2001
TIME: 21:17:44

INPUT SET: S36627.raw

46
47

(C) TELEX:

ERRORED SEQUENCES FOLLOW:

48 (2) INFORMATION FOR SEQ ID NO:1:

49

50 (i) SEQUENCE CHARACTERISTICS:

51

(A) LENGTH: 1560 base pairs

52

(B) TYPE: nucleic acid

53

(C) STRANDEDNESS: double strand

54

(D) TOPOLOGY: linear

55

56 (ii) MOLECULE TYPE: cDNA

57

58 (vi) ORIGINAL SOURCE:

59

(A) ORGANISM: enterovirus enterovirus type 71 (BrCr)

60

61 (IX) Feature:

62

(A) NAME/KEY:

63

(B) LOCATION:1..1560

64

65

66 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

67

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68 ttaaaacagc tgtgggttgt caccaccca Cagggtccac tgggcgctag tacactggta 60
69 tctcggtacc tttgtacgcc tgttttatac Cccctccctg atttgcaact tagaagcaac 120
70 gcaaaccaga tcaatagtag gtgtgacata Ccagtcgcat cttgatcaag cacttctgta 180
71 tccccggacc gagtatcaat agactgtgca cacgggttgaa ggagaaaacg tccgttaccc 240
72 ggctaactac ttcgagaagc ctagtaacgc cattgaagtt gcagagtgtt tgcctcagca 300
73 ctccccccgt gtagatcagg tcgatgagtc accgcattcc ccacgggcca ccgtggcggt 360
74 ggctgcggtt gcggcctgcc tatggggtaa cccataggac gctctaatac ggacatggcg 420
75 tgaagagtct attgagctag ttagtagtcc tccggcccct gaatgcggct aatcctaact 480
76 gcgagacaca tacccttaat ccaaagggca gtgtgtcgta acgggcaact ctgcagcgga 540
77 accgactact ttgggtgtcc gtgtttcttt ttattcttgt attggctgct tatggtgaca 600
78 attaaagaat tgttaccata tagctattgg attggccatc cagtgtcaaa cagagctatt 660
79 gtatatctct ttgttggatt cacacctctc actcttgaaa cgttacacac cctcaattac 720
80 attatactgc tgaacacgaa gcgatgggct cccaggtctc cacacagcga tccggctcgc 780
81 atgagaattc caactcagcc acggaaggct ccactataaa ttacacaacc attaattact 840
82 acaaagactc gtatgctgcc actgctggaa agcaaagtct caaacaagat cctgacaagt 900
83 ttgcgaaccc tgtgaaggac atctttactg aaatggcagc gcccttaaag tctccctctg 960
84 ctgaagcatg tggctatagc gaccgagtgg cacagcttac cattggaaat tccaccatta 1020
85 ctacacaaga agcagcaaac ataatagttg ggtatggtga gtggccttca tactgctctg 1080
86 ataatgatgc aacagcggta gacaaacctc cacggcctga tgtctcagta aatagatatt 1140
87 acacgctaga cactaagcta tgggagaaat catccaaggg gtgggtactg aagttcccag 1200
88 atgtactgac tgaaccggga gtttttggtc caaatgcaca atttcactac ttataccggt 1260
89 cagggttctg catccacgtt caatgtaacg ctagcaaat tccaccaagg gcgctactcg 1320
90 ttgcggtatt gcccgagtat gtcattggaa cagtggcagg cggcacaggc acagagaaca 1380
91 gtcacctctc ttataaaca acccaaccgg gcgctgatgg atttgaatta caacatccat 1440
92 atgttcttga tgctggaatt ccaatatctc agttgacagt gtgccctcac cagtggatca 1500

```

Do not include identifiers with no response. This feature is not mandatory.

nucleic bases should be in upper case.

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/724,678DATE: 05/03/2001
TIME: 21:17:45

INPUT SET: S36627.raw

93 atttacgaac caacaattgt gccaccataa tagtgccata catgaacaca ctaccttttg 1560
94

155 (2) INFORMATION FOR SEQ ID NO:6:
156

157 (i) SEQUENCE CHARACTERISTICS:

--> 158 (A) LENGTH: 20 bases
159 (B) TYPE: nucleic acid
160 (C) STRANDEDNESS: single
161 (D) TOPOLOGY: linear
162

163 (ii) MOLECULE TYPE: synthetic DNA
164

165 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
166

--> 167 ggttggttrst ggaarttⁱcc *i (inosine) is not to be 20*
168 *included in the sequence. It must be represented*
169 *by "n".*

200 (2) INFORMATION FOR SEQ ID NO:9:
201

202 (i) SEQUENCE CHARACTERISTICS:

--> 203 (A) LENGTH: 20 bases
204 (B) TYPE: nucleic acid
205 (C) STRANDEDNESS: single
206 (D) TOPOLOGY: linear
207

208 (ii) MOLECULE TYPE: synthetic DNA
209

210 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
211

--> 212 arrttⁱatcc aytgrtⁱgg → *Inosine is to be represented 20*
213 *by an "n" in the sequence.*
214

305 (2) INFORMATION FOR SEQ ID NO:16:
306

307 (i) SEQUENCE CHARACTERISTICS:

308 (A) LENGTH: 30 bases
309 (B) TYPE: nucleic acid
310 (C) STRANDEDNESS: single
311 (D) TOPOLOGY: linear
312

313 (ii) MOLECULE TYPE: synthetic DNA
314

315 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
316

317 cctacgccac tacacagcct ggtcagggtg
318
319

30

- 16 sequences shown
- 11 listed on page 1

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/724,678

DATE: 05/03/2001
TIME: 21:17:45

INPUT SET: S36627.raw

Line	Error	Original Text
14	Number of Sequences (11) Doesn't Equal Actual Count (16)	(iii) NUMBER OF SEQUENCES: 11
28	Mandatory Value Not Present	(D) SOFTWARE:
62	Unknown or Misplaced Identifier	(A) NAME/KEY:
63	Unknown or Misplaced Identifier	(B) LOCATION:1..1560
158	Entered (20) and Calc. Seq. Length (18) differ	(A) LENGTH: 20 bases
167	Wrong Nucleic Acid Designator	ggitggtrst ggaartticc
167	Wrong Nucleic Acid Designator	ggitggtrst ggaartticc
167	# of Sequences for line conflicts w/ running total	ggitggtrst ggaartticc
203	Entered (20) and Calc. Seq. Length (18) differ	(A) LENGTH: 20 bases
212	Wrong Nucleic Acid Designator	arrttiatcc aytgrtgigg
212	Wrong Nucleic Acid Designator	arrttiatcc aytgrtgigg
212	# of Sequences for line conflicts w/ running total	arrttiatcc aytgrtgigg

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/09/724,678

DATE: 05/03/2001
TIME: 21:17:45

INPUT SET: S36627.raw

CLASSIFICATION

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/09/724,678

DATE: 05/03/2001
TIME: 21:17:45

INPUT SET: S36627.raw

Line	Original Text	Corrected Text
3	(1) General Information	(1) GENERAL INFORMATION:
5	(i) APPLICANTS: Kang-Hung Lee	(i) APPLICANT: Kang-Hung Lee
11	(ii) TITLE OF THE INVENTION: METHODS FOR D	(ii) TITLE OF INVENTION: METHODS FOR DETECTIN